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## OM protein - protein search, using sw model

Run on: July 1, 2003, 17:48:35 ; search time 42 Seconds  
(without alignments)  
929.299 Million cell updates/sec

Title: US-09-782-587B-1

Perfect score: 2187

Sequence: 1 ANAFLXXLRLPGSLKRXCKXX.....LQKLMRSEPRPGVLLRAPFP 406

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 28324 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 28324

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73;\*

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	2167	99.1	466	1 KPHU7	coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
2	1601	73.2	443	2 146932	C;Species: Homo sapiens (man);C;Accession: 19-May-1989 #sequence_revision 19-May-1994 #text_change 08-Dec-2000
3	1566	71.6	407	1 KFB07	C;Accession: A28322; A23819; A31186; B31186; S63524
4	858.5	39.3	475	1 EXCH	R;O'Hara, P.J.; Gint, J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; M
5	858.5	39.3	488	1 EXH	Proc. Natl. Acad. Sci. U.S.A. 84: 5158-5162, 1987
6	850.9	38.9	416	1 KFB0	A;Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dep
7	843	38.5	492	1 EXBO	A;Reference number: A28322; PMID:8260948; PMID:3037537
8	831.5	38.0	482	1 EXRT	A;Accession: A28322
9	824	37.7	459	1 A0419	A;Molecule type: DNA
10	821	37.5	452	1 A30351	A;Residues: 1-466 <HAG>
11	781	35.7	461	1 KPHU	A;Cross-references: GB:J02933; NID:9180333; PIDN:AAA51983; 1; PRB:g180334
12	775	35.4	461	1 S18994	R;Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Sari, G.C.; Woodbury, R.G.; Hart
13	769	35.2	461	1 JX0210	A;Title: Characterization of a cDNA coding for human factor VII.
14	749	34.2	456	1 KXBO	A;Reference number: A23819; MUID:86205965; PMID:3486420
15	726	33.2	461	1 KXHU	A;Accession: A23819
16	519.5	23.8	275	2 I46712	A;Molecule type: protein
17	515.5	23.6	282	2 I48421	A;Residues: 61-212 <THI>
18	513.5	23.5	271	2 I46580	A;Accession: B31186
19	511	23.4	285	2 I48144	A;Molecule type: protein
20	509.5	23.3	274	2 I47078	A;Residues: 213-466 <TH2>
21	473	21.6	638	1 KOMSP1	R;Björn, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiya, Y.; Pe
22	461.5	21.1	638	1 KQTRPL	J. Biol. Chem. 266: 11051-11057, 1991
23	459.5	21.0	638	1 KQHUP	A;Title: Human Plasma and recombinant factor VII. Characterization of O-glycosylation
24	455.5	20.4	343	1 A57014	A;Reference number: A40529; MUID:9125011; PMID:1904059
25	444	20.3	625	1 KFHUI	A;Comments: annotation: carbohydrate binding sites
26	443.5	20.3	622	1 TBHU	R;Personn, E.; Petersen, L.C.
27	439.5	20.1	655	1 A46688	Eur. J. Biochem. 224: 293-300, 1995
28	428.5	19.6	625	1 TBBO	A;Title: Structurally and functionally distinct $\text{Ca}^{2+}$ binding sites in the gamma-car
29					A;Reference number: S63524; MUID:96096752; PMID:8529655

## ALIGNMENTS

30	428	19.5	1035	1 A43090	enteropeptidase (E trypsin (EC 3.4.21.1)
31	426.5	19.5	246	1 TRT1	thrombin (EC 3.4.2
32	425.5	19.5	618	2 A35627	trypsin (EC 3.4.21.1)
33	423	19.3	229	1 TRDS	trypsin (EC 3.4.21.1)
34	423	19.3	558	2 JC878	plasma hyaluronan-thrombin (EC 3.4.2
35	421	19.3	617	2 S10511	trypsin (EC 3.4.21.1)
36	420.5	19.2	247	2 A27547	enteropeptidase (E serine proteinase
37	418	19.1	1019	1 A53318	enteropeptidase (E trypsin (EC 3.4.21.1)
38	417	19.1	786	1 A7547	hepsin (EC 3.4.21.1)
39	417	19.1	1034	1 A56663	membrane-bound arg
40	416.5	19.0	246	1 TRR12	membrane-type-1 hepsin (EC 3.4.21.1)
41	415.5	19.0	855	2 JC7731	trypsin (EC 3.4.21.1)
42	415	19.0	855	2 JC7731	plasmin (EC 3.4.21.1)
43	413	18.9	417	1 S00845	trypsin (EC 3.4.21.1)
44	412.5	18.9	248	2 S55066	plasmin (EC 3.4.21.1)
45	411	18.8	810	2 I46260	plasmin (EC 3.4.21.1)

A;Pathway: blood coagulation extrinsic pathway  
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl  
 F;1-20/Domain: signal sequence #status predicted <S>  
 F;21-50/Domain: propeptide #status predicted <PRO>  
 F;45-104/Domain: Gla domain homology <GLA>  
 F;110-141/Domain: EGF homology <EGI>  
 F;151-187/Domain: EGF homology <EG2>  
 F;213-446/Product: coagulation factor VIIa heavy chain #status experimental <MA1>  
 F;213-447/Domain: trypsin homology <TRY>  
 F;66,67,74,67,79,80,85,86,89,93/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental  
 F;82,110-121,115-130,132-141,151-162,158-172,174-187,195-222,219-224,238-254,370-389,  
 F;112-120/Binding site: carbohydrate (Ser) (covalent) #status experimental  
 F;205,382/Binding site: erythro-beta-hydroxyaspartic acid (Asp) #status absent  
 F;212-213/Cleavage site: Arg-Ile (coagulation factor XIA) #status experimental  
 F;253,302,404/Active site: His, Asp, Ser #status predicted  
 F;350,351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 99.1%; Score 2167; DB 1; Length 466;  
 Best Local Similarity 97.5%; Pred. No. 4.4e-154;  
 Matches 396; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 1 ANAFLXXLRPGSLXKCKXXCSFXKARXIFKDAKXTKLFWISYSGDQASSPONGGS 60  
 61 ANRFLLELRPGSLERECKEEKSFEAREIFKDAERTKLFWISYSQGDQASSPONGGS 120  
 Oy 61 CRKDQSYVICFLPAFGRGRNCETHKDQDOLICVNENGCEQCSDHGTGKSRCHEGYSL 120  
 121 CRKDQSYVICFLPAFGRGRNCETHKDQDOLICVNENGCEQCSDHGTGKSRCHEGYSL 180  
 Db 121 LADGVSCPTVYPGKIPILEKRNAKPOGRIVGKVCPKGECPMQVLLVNGAQLCGG 180  
 181 LADGVSCPTVYPGKIPILEKRNAKPOGRIVGKVCPKGECPMQVLLVNGAQLCGG 240  
 Oy 181 TLINTINWVSAAHCFDKIKNNRNLIAVLGEHDLSERHDGEOSRRVAQVIIPTSTYPTGN 240  
 241 TLINTINWVSAAHCFDKIKNNRNLIAVLGEHDLSERHDGEOSRRVAQVIIPTSTYPTGN 300  
 Oy 241 HDIALLRLHQPVTLTDRVPLCPKIPILEKRNAKPOGRIVGKVCPKGECPMQVLLVNGAQLCGG 300  
 Db 301 HDIALLRLHQPVTLTDRVPLCPKIPILEKRNAKPOGRIVGKVCPKGECPMQVLLVNGAQLCGG 360  
 361 IVSWGOCATVGHFGVYTRVSQYIENIQKLARSEPRPGVLLRAPF 406  
 Db 361 IVSWGOCATVGHFGVYTRVSQYIENIQKLARSEPRPGVLLRAPF 406  
 Db 399 VWSWGECCARVGHFGVYTRVSOIENIQLMRSEPRPGVLLRAPF 443

RESULT 2

Oy Query Match 73.2%; Score 1601; DB 2; Length 443;  
 Best Local Similarity 71.4%; Pred. No. 6.4e-112;  
 Matches 290; Conservative 42; Mismatches 72; Indels 2; Gaps 2;

Oy 1 ANAFLXXLRPGSLXKCKXXCSFXKARXIFKDAKXTKLFWISYSGDQASSPONGGS 60  
 40 ANSFLBLRPGSLERECKEELCSFEEAREVFOSTERKIQFWMITYNDGDOCAASNPGGS 99  
 Db 61 CKDQSYVICFLPAFGRGRNCETHKDQDOLICVNENGCEQCSDHGTGKSRCHEGYSL 120  
 100.CEDQSYVICFLPAFGRGRNCETHKDQDOLICVNENGCEQCSDHGTGKSRCHEGYSL 159  
 Oy 121 LADGVSCPTVYPGKIPILEKRNAKPOGRIVGKVCPKGECPMQVLLVNGAQLCGG 180  
 160 LPNGVSCPTVYPGKIPALEKRGASNPQGRIVGKVCPKGECPMQVLLVNGAQLCGG 219  
 Db 181 TLINTINWVSAAHCFDKIKNNRNLIAVLGEHDLSERHDGEOSRRVAQVIIPTSTYPTGN 240  
 220 SLDDTHWVNSAHCDFDKLSSLNLNTLVLGEDLSERHDSEHGEDEVVRHAQOLIMEDKYYPGKT 279  
 Oy 241 HDIALLRLHQPVTLTDRVPLCPKIPILEKRNAKPOGRIVGKVCPKGECPMQVLLVNGAQLCGG 180  
 280 HDIALLRLHQPVTLTDRVPLCPKIPILEKRNAKPOGRIVGKVCPKGECPMQVLLVNGAQLCGG 339  
 Oy 301 NPRLMTQDCIQLQSKRKGDSNITEVMFCAGYSDGSKDSCKDSCGDSSGPATHYRGWTLG 360  
 340 DVPRLMQDCEVEOSEHNPGSSEVTGNGMFCAGYLDSSKACKGDSGPATHYGT-YLTG 398  
 Db 361 IVSWGOCATVGHFGVYTRVSQYIENIQKLARSEPRPGVLLRAPF 406  
 Db 399 VWSWGECCARVGHFGVYTRVSOIENIQLMRSEPRPGVLLRAPF 443

RESULT 3

KFB07 coagulation factor VIIa (EC 3.4.21.21) - bovine  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999  
 C;Accession: A11979; C2074  
 R;Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.  
 J. Biol. Chem. 263, 14868-14877, 1988  
 A;Title: Bovine factor VII. Its purification and complete amino acid sequence.  
 A;Reference number: A11979; PMID:8908362; PMID:3049594  
 A;Accession: A11979  
 A;Molecule type: protein  
 A;Residues: 1407 <TM>  
 R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood  
 A;Reference number: A20274; PMID:8308813; PMID:6688526  
 A;Accession: C20274  
 A;Molecule type: Protein  
 A;Residues: 58-62, X, 64-68 <MC>  
 A;Note: the residue designated 'X' was determined to be hydroxyaspartic acid  
 R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanag  
 J. Biochem. 104, 867-868, 1988  
 A;Title: A new triosephosphate sugar chain linked to a serine residue in bovine blood c  
 A;Reference number: A44556; PMID:89213999; PMID:3149637  
 A;Contents: annotation  
 A;Note: structure and location of covalently bound carbohydrate  
 C;Function:  
 A;Description: catalyzes the proteolytic activation of coagulation factor X in the pr  
 gulation factor IX in the presence of calcium and tissue factor  
 A;Pathway: blood coagulation extrinsic Pathway  
 A;Molecule type: mRNA  
 A;Residues: 1-443 <BRC>  
 A;Cross-references: GB:SS56300; NID:9266294; PID:9266295  
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 F;24-83/Domain: Gla domain homology <GLA>  
 F;189-210/Domain: EGF homology <EG1>  
 F;130-166/Domain: EGF homology <EG2>  
 F;192-425/Domain: trypsin homology <TRY>

F;6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status F;17,22,50-61,55-70,71-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/ F;52/Binding site: carbohydrate (Ser) (covalent) #status experimental  
 F;63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental  
 F;145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;153-153/Cleavage site: Arg (Ile (Coagulation factor XIA)) #status experimental  
 F;193,242,344/Active site: His, Asp, Ser #status predicted  
 F;290-291/Cleavage site: Arg-Gly (Coagulation factor Xa) #status experimental  
 Query Match 71.6%; Score 1566; DB 1; Length 407;  
 Best Local Similarity 69.6%; Pred. No. 2.4e-109; Mismatches 75; Indels 0; Gaps 0;  
 Matches 275; Conservative 45; Mismatches 75;  
 Qy 1 ANAFLXXLRPGSLRXCKXQCCFXXARXIKDXRTKLFWISYSQDGCASSRCQNGS 60  
 Db 1 ANGLEELLEPLPSLRECREBELCSEAHIFRNBERTOFWQNSYNDGDOCASSPCONGS 60  
 Qy 61 CKDQLQSYICFCIPAFEGRNECHKDQOLIVCENGGBQYCSDHGTGKRSJCRCHEGL 120  
 Db 61 CEBQLRSYICFCPDGFEGRCNCTDKDOSLICANDNGGEQYCCADPGAGRCFCHEGYL 120  
 Qy 121 LADGVSCPTVEPPCGKIPILEKRERNASKPQGRITVGKVCPKGCPWQVILLVNGAQLCGG 180  
 Db 121 QADGVSCAPTEVPCPKGKIPVLERNGSKPQGRIVGGHCPKGCPWQAMKLKLNGG 180  
 Qy 181 TINTTIIWVSAACFDKIKNWRILIAVIGEHDSEHDQDEOSIRVAQVITSPYVPGTN 240  
 Db 181 TLVGPWAVTVAACIFERLRSRGNLATVIGEHDLSRVPEQEPRQVRAQIVPKVQVPGND 240  
 Qy 241 HDTALLRLHQPVLTDHVPLCIPPERFSERTLAFLVRSLSVWSQGQLLDRGTALEALV 300  
 Db 241 HDVALLQLAQPVLPALCLDPFDADOTLAFVRLSAVSGWOLLERGVARKLAVY 300  
 Qy 301 NVRPLMQDCLOOSRKVKGDSPLNITEYMFCAGYSSDGSKOSCKGSGGGPHATHYGTWYLG 360.  
 Db 301 LVPRLLRQDCLOOSRKVQPGPVWTDNMFCAGYSSDGSKDACKGSGGGPHATRFGTWELTG 360  
 Qy 361 IVSWGQGATVFRGVTRVSOQTEWQKLMRSEP 395  
 Db 361 IVVSGEGCAAGHFGIVTRVSRYTAWLRLQLMGHPP 395  
 Result 4  
 EXCH coagulation factor Xa (EC 3.4.21.6) precursor - chicken  
 N;Alternate names: virus-activating proteinase  
 C;Species: Gallus gallus (chicken)  
 C;Date: 12-Feb-1993 #sequence\_revision 07-Feb-1997 #text\_change 16-Jul-1999  
 C;Accession: S15838; S2030; S0381  
 R;Suwaki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na  
 FBS Lett. 283, 281-285, 1991  
 R;Ogasawara, T.; Na  
 FBS Lett. 278, 1992  
 A;Title: Primary structure of the virus activating protease from chick embryo. Its ident  
 A;Reference number: S15838; MUID:91257322; PMID:204767  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-75 <S02>  
 A;Cross-references: DDBJ:00844; NID:922869; PIDN:BA00724.1; PID:9222870  
 R;Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.  
 FBS Lett. 296, 274-278, 1992  
 A;Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsible  
 A;Reference number: S20380; MUID:92164779; PMID:1537403  
 A;Molecule type: Protein  
 A;Residues: 41-55 <G02>  
 A;Accession: S20381  
 A;Molecule type: Protein  
 A;Residues: 241-246, X', 248-251, X', 253-261 <G07>  
 C;Function:  
 A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A;Pathway: blood coagulation  
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-40/Domain: propeptide #status predicted <PRO>  
 F;52-84/Domain: GlA domain homology <GLA>  
 F;41-485/Product: coagulation factor X light chain #status experimental <LCX>  
 F;90-121/Domain: EGFR homology <EG3>  
 F;129-167/Domain: EGF homology <EG2>  
 F;186-240/Domain: activation peptide #status predicted <APM>  
 F;241-475/Product: coagulation factor Xa heavy chain #status experimental <HXC>  
 F;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu)  
 F;55-62,90-101,95-110,112-121,128-140,136-152,154-167,175-348,247-252,267-283,396-410  
 F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F;196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;282,328,425/Active site: His, Asp, Ser #status predicted  
 Query Match 39.3%; Score 856.5; DB 1; Length 475;  
 Best Local Similarity 37.3%; Pred. No. 1.e-56; Mismatches 136; Indels 67; Gaps 8;  
 Matches 157; Conservative 75; Mismatches 136; Indels 67; Gaps 8;  
 Qy 1 ANAFLXXLRPGSLRXCKXQCCFXXARXIKDXRTKLFWISYSQDGCASSRCQNGS 60  
 Db 41 ANSFLEEMQNIERECBNCREEAREAFEDNEKTEFWNTVQDQCSNSPCHYGG 100  
 Qy 61 CKDQLQSYICFCIPAFEGRNECHKDQOLIVCENGGBQYCSDHGTGKRSJCRCHEGL 115  
 Db 101 CKDGGSYMCSCLDQYQGKNEF----VTPYCKINNGDCBQFCSIKKSVQDVKVQSC 155  
 Qy 115 EGYSLLADQSYCPTVEPPCGKI-----PILEKRNASKPQG----- 151  
 Db 155 SGYSLAEDQKOCVSKVQPKVGMKRRKSVLPIVNTNTSDQVPTSPSTGNSLIEFW 215  
 Qy 152 -----RIVSGKVCPKGCPWQ-VILLVNGAQLCGGTLNTI 186  
 Db 215 TTTEESPPIPPIPNSSITDPNVDTIVGDECRCGECPCPWQAVLINEKEFGCGTILND 275  
 Qy 187 WVSAAHCDCDKIKNWRILIAVIGEHDSEHDQGEQSRAVQVITSPYVPGTNHDALL 246  
 Db 276 FILTAHCINQSK---EIRKVVGEVDREKEEHSSETHTAAKIFVHSKYTAETYDNDALL 332  
 Qy 247 RLHOPVLTDHVPLCBLRTFSERTLAFLVRSLSVWSQGQLLDRGATALLAVLNVRML 306  
 Db 333 KLKPIRQPSSEYVYPAQDQAEENLVNLNQKSMWSSRGEEGRASRKLKVLEVYWD 392  
 Qy 307 TQDCLQSYRKGDSPLNITEYMFCAGYSSDGSKOSCKGSGGGPHATHYGTWYLG 366  
 Db 393 RSTCKQSTNFA----IEFMFCAGIEETQKDACQGDGGPHVTRYKOTYFTVGIWSGE 447  
 Qy 367 GCATVGHGCVYVTRVSOQYKIVLWKLMRSE 394  
 Db 448 GCARKGKGYQYTKLRLRWRVTVMRQK 475  
 Result 5  
 EXJO coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human  
 N;Alternate names: Stuart factor  
 C;Species: Homo sapiens (man)  
 C;Date: 15-Nov-1984 #sequence\_revision 02-May-1994 #text\_change 08-Dec-2000  
 C;Accession: A24778; J00917; A45485; A25533; A22208; A21284; A20362; S39415; I54051;  
 R;Levyt, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.  
 Biochemistry 25, 5098-5102, 1986  
 A;Title: Gene for human Factor X, a blood coagulation factor whose gene organization  
 A;Reference number: A24478; MUID:87026600; PMID:3768336  
 A;Accession: A24478  
 A;Molecule type: DNA  
 A;Residues: 1-488 <LET>  
 A;Cross-references: GB:L29433; GB:M14327; NID:9459809; PIDN:AAA52764.1; PID:9182831  
 R;Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.  
 Gene 99, 291-294, 1991  
 A;Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human c  
 A;Reference number: J00917; MUID:91216473; PMID:1902434  
 A;Accession: J00917

A; Molecule type: mRNA  
A; Residues: 1-488 <MES>  
A; Cross-references: GB:457285; NID:9182389; PIDN:AA52421.1; PIB:9182390  
R; Mao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.  
J. Biol. Chem. 267, 7305-7401, 1992  
A; Title: Liver-specific expression of the gene coding for human factor X, a blood coagulation protein  
A; Reference number: A41485; MUID:92218390; PMID:1313796  
A; Accession: A42485  
A; Molecule type: DNA  
A; Residues: 1-15 <MA>  
A; Experimental source: liver  
A; Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBIPI:93787)  
R; Haul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.  
A; Reference number: A25853; MUID:86221713; PMID:3011603  
A; Accession: A25853  
A; Molecule type: mRNA  
A; Residues: 19-284 '>E' 289-488 <RAU>  
A; Cross-references: GB:M2613; NID:9180335; PIDN:AA51984.1; PIB:9180336  
R; Fung, M.R.; Hay, C.W.; Macmillivray, R.T.A.  
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985  
A; Title: Characterization of an almost full-length cDNA coding for human blood coagulation protein  
A; Reference number: A22208; MUID:85216545; PMID:2582420  
A; Accession: A22208  
A; Molecule type: mRNA  
A; Residues: 13-441, 'S' 443-488 <FUN>  
A; Cross-references: GB:K03194; NID:9182840; PIDN:AA52490.1; PIB:9182841  
R; Leytus, S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 81, 3690-3702, 1984  
A; Title: Characterization of a cDNA coding for human factor X.  
A; Reference number: A21284; MUID:84222026; PMID:6587384  
A; Molecule type: mRNA  
A; Residues: 13-204, '>E' 289-488 <LE2>  
A; Cross-references: GB:K01866  
R; McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weins Biochemistry 22, 2875-2884, 1983  
A; Title: Complete amino acid sequence of the light chain of human blood coagulation factor X.  
A; Reference number: A20362; MUID:83257207; PMID:6871167  
A; Accession: A20362  
A; Molecule type: protein  
A; Residues: 41-179 <NCW>  
R; Inoue, K.; Morita, T.  
Eur. J. Biochem. 218, 153-163, 1993  
A; Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
A; Reference number: S39414; MUID:94062825; PMID:8243461  
A; Accession: S39415  
A; Molecule type: protein  
A; Residues: 183-234 <INO>  
A; Note: glycosylation sites  
A; Note: identification and characterization of beta-hydroxyaspartic acid  
R; Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhuhanam, K.; Lyman, G.  
Gene 84, 517-519, 1999  
A; Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human  
A; Reference number: 154051; MUID:90128299; PMID:2612918  
A; Accession: I54051  
A; Status: translation not shown; translated from GB/EMBL/DDJB  
A; Residues: 1-233 <RES>  
A; Cross-references: GB:M33297; NID:9183860; PIDN:AAA52636.1; PIB:955330  
R; Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bla J. Mol. Biol. 232, 947-966, 1993  
A; Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
A; Reference number: A49558; MUID:93360277; PMID:8355279  
A; Contents: annotation, X-ray crystallography, 2.2 angstroms  
C; Comment: The two chains held together by one disulfide bond are formed from a single-chain peptide. The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or  
C; Genetics:  
C; Pathway: blood coagulation  
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylic acid; signal sequence #status predicted <SIG>  
F; 1-27/Domain: signal sequence #status predicted <SIG>  
F; 24-40/Domain: proteptide #status predicted <PRO>  
F; 25-84/Domain: propeptide #status predicted <PRO>  
F; 41-179/Product: coagulation factor X light chain #status experimental <LCX>  
F; 90-121/Domain: EGF homology <EG2>  
F; 183-488/Domain: activation factor X heavy chain #status experimental <HCH>  
F; 235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>  
F; 235-462/Domain: trypsin homology <TRY>  
F; 46-47, 54, 55, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxyglutamic acid (Glu) #  
F; 57-62/Disulfide bonds: #status predicted  
F; 70-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-342, 241-246, 261-277, 390-404, 415-416/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F; 199, 211/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F; 221, 230/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F; 234-235/Cleavage site: Argile (coagulation factor IXa, coagulation factor VIIa) #  
F; 276, 322, 419/Active site: His, Asp, Ser #status experimental

Query Match 39 3%; Score 858.5; DB 1; Length 488;  
Best Local Similarity 37.1%; Pred. No. 1.5e-56;  
Matches 168; Conservative 76; Mismatches 146; Indels 63; Gaps 8;  
QY 1 ANAEFLXLRLRGLSLRXRXQXXQCSFXARXFKDAXRTKFQWISSSDGDCASSPQONGGS 60  
Db 41 ANSEELLEMKGKHLEECMECTSYEARDEVFEDSKTNEPWKVKGDQOCETSFQCONQK 100  
QY 61 CKDQIQ-QSYVCFCLPAFEGRNC--THKDDPOLYCNGCSEQYQSDHTGCKRSRCHEGY 118  
Db 101 CKDGIGEVYCYTCLEGEPEGKNCLETRK---LCSLDNGDODFFKEEQNS-VQSCARGY 155  
QY 119 SLLADGVSTPTVEVPCGKIPILERKRNASKPQG----- 151  
Db 156 TLADNGKACIPTGPYPCGK-QTLERKRKRSVAQTSSSGEAPDSITWKPKYDAADLDPTEP 214  
QY 152 -----RIVGKVCPRGECPPQVLL-VNGQLCGGTINTIWVVA 191  
Db 215 FDLDLFNQTOPERGDDNNLTFRIVGQCECKGCPWQVLA 274  
QY 192 AHCFDRKKIWKRNLTAVLGSDHLDSEHDLSDGDSQRSSRYAQVILPSTVPGTTNHDIALLRLHQP 251  
Db 275 AHCIQXAKRFK--WRVGRDNTEDOEEGGERAVHEVEVVVKHRNRTKETIDFDIAVLRKMP 331  
QY 252 VVLTDDHVYPLCLPERTSERTLAFRVPLSVGQNLQDRTGATEALMLVNPRIMTQCL 311  
Db 332 ITFRMKNVAPACPLPERDWASTLMTQTKGIVSGFGFRTHEKGROSTTRKALEPVYDVRNSC- 390  
QY 312 QOSRKVGSPNITEYMFAGYSQDSGSKDSCKGDGGPHATHYRGTYLWLGIVSNGCCATV 371  
Db 391 ---KLSSSFITQNMFCAGYDQKEDACQGDGGPHVTRFKDTYFVIGIVSNGECAK 446  
QY 372 GHGVGVYTRVSQYEWLOKLMRSPRPVYLRA 404  
Db 447 GKYGIGYTRVAFKWKIDRSMKTRGPKRAKSHP 479  
RESULT 6  
KFB0 coagulation factor IXa (EC 3.4.21.22) precursor - bovine  
N; Alternate names: Christmas factor  
C; Species: Bos primigenius taurus (cattle)  
C; Date: 30-Nov-1980 #sequence\_revision 03-Aug-1984 #text\_change 16-Jul-1999  
C; Accession: A14757; B20274; J15891; A00823  
R; Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979  
A; Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas  
A; Reference number: A14757; MUID:80056619; PMID:291916



A;Title: Isolation and characterization of a cDNA coding for human factor IX.  
A;Accession: A30623; MUID:83065193; PMID:6959130  
A;Molecule type: mRNA  
A;Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',  
A;Cross-references: GB:J00136; NID:9182608; PID:AAH9726.1; PID:9182609  
A;Experimental source: liver  
R;Marakhan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.;  
Vox Sang. 58, 21-29, 1990  
A;Title: Development of an immunoaffinity process for factor IX purification.  
A;Accession: A60486; MUID:90194857; PMID:2316207  
A;Molecule type: protein  
A;Accession: A20274  
A;Molecule type: protein  
A;Residues: 105-109, 'X', 111-115 <NCM>  
R;Bolland, A.; Faure, T.; Carvalho, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Salle, Eur. J. Biochem. 172, 565-572, 1988  
A;Title: Characterisation of two differently processed forms of human recombinant factor IX; Reference number: S02527; MUID:88166735; PMID:3280312  
A;Accession: S02527  
A;Molecule type: protein  
A;Residues: 29-63 <BAL>  
A;Note: processed forms expressed in recombinant system  
R;Jallat, S.; Perraud, F.; Dalemans, W.; Bolland, A.; Dieterle, A.; Faure, T.; Meulien, EMBQ J. 9, 3295-3301, 1990  
A;Reference number: S12058; MUID:91006024; PMID:2209546  
A;Molecule type: mRNA; protein  
A;Residues: 1-68 <JAL>  
A;Note: processed forms expressed in recombinant system  
R;Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbell, EMBQ J. 9, 475-480, 1990  
A;Title: The first EGF-like domain from human factor IX contains a high-affinity calcium A;Reference number: S12377; MUID:90151623; PMID:2405129  
A;Accession: S12377  
A;Molecule type: protein  
A;Residues: 92-130 <HAN>  
A;Note: NMR detection of calcium binding by domain expressed in recombinant system  
R;de la Salle, C.; Charmantier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum, Thromb. Haemost. 70, 370-371, 1993  
A;Title: A deletion located in the 3' non translated part of the factor IX gene responsi A;Accession: 159612; MUID:94054330; PMID:8236150  
A;Accession: 159612  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 44-461 <RES>  
A;Cross-references: GB:560752; NID:9439773; PIDN:AB28598.1; PID:9439774  
R;Stoflet, E.S.; Koehler, D.D.; Sarkar, G.; Sommer, S.S.  
Science 219, 491-494, 1988  
A;Title: Genomic amplification with transcript sequencing.  
A;Reference number: 159529; MUID:88127096; PMID:3340835  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 290-359 <REQ>  
A;Cross-references: GB:M19063; NID:9182622; PIDN:AAA52456.1; PID:9182623  
R;Ararwala, K.L.; Kawabata, S.; Takao, T.; Morata, H.; Shimomishi, Y.; Nishimura, H.; Iw Biochemistry 33, 5167-5171, 1994  
A;Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin A;Accession: A54555; MUID:94227047; PMID:8172892  
A;Accession: A54255  
A;Molecule type: protein  
A;Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGt>  
A;Note: the residues designated 'X' were determined to be threonine bound to carbohydrate J. Clin. Invest. 61, 1528-1538, 1978

A;Title: Activation of human factor IX (Christmas factor).  
A;Reference number: A18483; MUID:78194509; PMID:659613  
A;Contents: annotation; activation; active site; carbohydrate binding  
R;McGrath, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D. Am. Soc. Hematol. Abstr. 64 (Suppl.1), 262a, 1984  
A;Reference number: A37569  
A;Contents: annotation  
R;Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.  
J. Biol. Chem. 259, 5698-5704, 1984  
A;Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-bindin A;Reference number: A37543; MUID:84185715; PMID:6435296  
A;Contents: annotation; calcium binding  
R;Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G. Cell 45, 343-348, 1986  
A;Title: Defective propeptide processing of blood clotting factor IX caused by mutati A;Reference number: A37555; MUID:86189947; PMID:3009023  
A;Contents: annotation; signal sequence cleavage site  
R;Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kar J. Biol. Chem. 264, 21257-21265, 1989  
A;Title: Blood clotting factor IX (B(M) Nagoya: substitution of arginine 180 by trypti A;Reference number: A30622; MUID:9078229; PMID:2929373  
A;Note: recombinant form expressed in yeast  
R;Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brk submitted to the Brookhaven Protein Data Bank, November 1991  
A;Contents: annotation; conformation by (1)H-NMR, residues 92-130  
C;Comment: Factor IX is activated by factor Xa, which excises the activation peptic C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with C;Genetics:  
A;Gene: GDB:F9  
A;Cross-references: GDB:119900; OMIM:306900  
A;Map position: Xg27.1-xq27.2  
A;Intron: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1  
C;Function:  
A;Description: catalyzes the proteolytic activation of coagulation factor X in the p A;Pathway: blood coagulation intrinsic pathway  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homo C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxygl F:1-28/Domain: signal sequence #status predicted <SGI>  
F:29-46/Domain: Propeptide #status experimental <PP>  
F:31-91/Domain: Gla domain homology <Gla>  
F:47-191/Domain: coagulation factor IXa light chain #status experimental <ALC>  
F:97-128/Domain: EGF homology <EG2>  
F:192-226/Domain: activation peptide #status experimental <ACT>  
F:227-461/Domain: coagulation factor IXa heavy chain #status experimental <ABC>  
F:227-454/Domain: trypsin homology <TRY>  
F:53, 54, 61, 63, 66, 67, 72, 73, 76, 79, 82, 86, 89, 92, 95, 97, 98, 100, 102, 107, 117, 119-128, 134-145, 141-155, 157-170, 179, 18-335, 252-268, 382-396, 407-4: F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental  
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:191-192/Cleavage site: Arg-Ala (coagulation factor IXa) #status experimental  
F:203-213/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:205, 215/Binding site: Arg-Val (coagulation factor IXa) #status experimental  
F:226-227/Cleavage site: Arg-Val (coagulation factor IXa) #status experimental  
Query Match  
Best Local Similarity 38.8%; Score 849; DB 1; Length 461;  
Matches 161; Conservative 71; Mismatches 132; Indels 50; Gaps 7;  
OY 11 GSLRKCKXXQCSFXARXKIDAXRKLFWISYSQDCASSPCQNGGSCKDOLASVYC 70  
Db 1 :|| | | :|| || :|| | | | | :|| | | | | :|| | | | | :|| |  
58 GNLERECMEKCSFSEAREREVENTERTERERFQKVQDGQDCESNPCLNGGSKCDINSYC 117  
OY 71 FCLPAFGRNCETHKDQDOLICVNENGSCQEYCSDHGTKRSRCRCHGSGYSSLLADGVCTPT 130

Db 118 WCPFFPEGRKNEEL---DVTCNIKNGRCQFCCKNSADNKVYVCSCIEGYRLAINNRSCEPA 173  
 Qy 131 VEYPCGKIPILEKRKASKPQG-----RIVGGKVC 159  
 Db 174 VPFRCGRVSOTSLRTRAVAPEPVDPYVNSTERAFTLDNTQSNTQSNDFTRVGGEDA 233  
 Qy 160 PKGEPPWQVLLVNAQLCGGTLLNITIWVAHCFDKTKRNWTAIVLGEEDSEHDGD 219  
 Db 234 KPGEPFWQVVLNGKVDACFGGSIVNEKWTAAHC--VETGVKITVVAEGHENITEHT 290  
 Qy 220 EQSRIVAQVITPVSTVPGT-----NDIATALLHPWPLTDVWVPCLPERFSEFLAFVR 277  
 Db 291 EOKRNVIRILPHHNNAATKYNHDIALLDELPELVNLNSVTPTCIAKD--EYNIFLK 347  
 Qy 278 F--SVLSGNGQLLRGATALELMVNLNVPRMTQDQLQSQSRKVGSNPNTIMFAGYSDG 335  
 Db 348 FGSGTVSGNGRVEFHGRSLALVLOVLRVPLDRATCLRSIKF---TYINNMFCAGFHEG 402  
 Qy 336 SKDSQKGDSGGPHATHYRGWLTIVSWSQGCAVVGHECVYTRVSOYEWLQK 389  
 Db 403 GRDSCQGDGGPHVTEVECTISFLGIISNGEECAMKGKIGIYTKVSRVWNIKE 456

**RESULT 8**

EXPO coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
 N;Alternate names: Stuart factor  
 C;Species: Bos primigenius taurinus (cattle)  
 C;Date: 24-Apr-1984 #sequence-revision 17-Mar-1987 #text-change 16-Jul-1999  
 C;Accession: A22867; A14997; A12030; A34412; S30414; A00925  
 R;Fung, M.R.; Campbell, R.M.; MacCollum, T.A.  
 Nucleic Acids Res 12, 4481-4492, 1984  
 A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
 A;Reference number: A22867; MUID:84247315; PMID:6330671  
 A;Accession: A22867  
 A;Molecule type: mRNA  
 A;Residues: 1-487 <FUN>  
 A;Cross-references: GB:X00673; NID:9192; PTDN:CAA25206.1; PID:9193  
 R;Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.  
 Biochemistry 19, 659-667, 1980  
 A;Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
 A;Reference number: A14997; MUID:8010563; PMID:6766735  
 A;Accession: A14997  
 A;Molecule type: protein  
 A;Residues: 41-102, N-104-180 <ENF>  
 R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor X-1 (Stuart factor).  
 A;Reference number: A0074; MUID:83350813; PMID:6688526  
 A;Contents: annotation; revision to residue 103  
 R;Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3062-3066, 1975  
 A;Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
 A;Reference number: A12030; MUID:76053069; PMID:105093  
 A;Accession: A12030  
 A;Molecule type: protein  
 A;Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-411, 'GKFG', 446-492 <ENF>  
 A;Note: carbohydrate binding sites and disulfide bonds were determined  
 R;Person, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.  
 J. Biol. Chem. 264, 16897-16904, 1989  
 A;Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
 A;Reference number: A34412; MUID:89380326; PMID:2789221  
 A;Molecule type: protein  
 A;Residues: 85-26 <PER>  
 A;Note: beta-hydroxyaspartic acid site  
 R;Inoue, K.; Morita, T. 1993  
 Eur. J. Biochem. 218, 153-163,  
 A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A;Reference number: S30414; MUID:94062825; PMID:8243461  
 A;Accession: S30414  
 A;Molecule type: protein

A;Residues: 183-196;199-209;216-233 <INO>  
 A;Note: carbohydrate binding site  
 R;Titani, K.; Hermansson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
 Biochemistry 11, 4839-4903 1972  
 A;Title: Bovine factor X-1a (activated Stuart factor): Evidence of homology with mammalian factor Xa  
 A;Reference number: A12033; MUID:1053314; PMID:426426  
 A;Contents: annotation; active site  
 R;Fujikawa, K.; Titani, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
 A;Title: Activation of bovine factor X (Stuart factor): conversion of factor Xalpha  
 A;Reference number: A1304; MUID:76053121; PMID:1059122  
 A;Contents: annotation; activation  
 R;Sugio, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
 J. Biol. Chem. 259, 5705-5710, 1984  
 A;Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamyl residue  
 A;Reference number: A38024; MUID:84185216; PMID:6546930  
 A;Contents: annotation; calcium binding  
 R;Morita, T.; Jackson, C.M.  
 J. Biol. Chem. 261, 4008-4014, 1986  
 A;Reference number: A38025; MUID:86140210; PMID:394900  
 A;Contents: annotation; sulfate binding  
 C;Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
 C;Comment: The two chains are formed from a single-chain precursor by the excision of activation peptide.  
 C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway)

C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with sulfate, to the gamma-carboxyglutamic acid residues arise by a posttranslational, via C;Genetics:

A;Gene: F10

A;Map position: 13q34

C;Function:

A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the blood coagulation pathway

C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl residue; signal sequence #status predicted <SIG>

F15-40/Domain: signal peptide #status predicted <PRO>

F21-84/Domain: Gla domain homology <GLA>

F41-180/Product: coagulation factor X light chain #status experimental <LCX>

F9-121/Domain: EGF homology <EGF>

F119-164/Domain: EGF homology <EG2>

F15-49/Domain: coagulation factor X heavy chain #status experimental <APX>

F163-233/Domain: activation peptide #status experimental <APX>

F214-492/Product: coagulation factor Xa heavy chain #status experimental <RHC>

F45-47-54,56-59,60-65,66,69-72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) F55-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status experimental

F20/0/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F20/0/Binding site: sulfate #status experimental

F208,485/Binding site: carbohydrate (Thr) (covalent) #status experimental

F218/Binding site: carbohydrate (Asn) (covalent) #status experimental

F223-234/Cleavage site: Arg-Tle (coagulation factor IXa, coagulation factor VIIa) #3

F240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental

F275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 38.5%; Score 843; DB 1; Length 492;  
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 Matches 165; Conservative 147; Indels 56;

Qy 1 ANALXXLRRPLSLRXXXXCSRXARXIFKDXRKLFWISYSGDQCCSPCQNGS 60  
 Db 41 ANSFLEEVKGQNLRERECCEAACLEEARFEDEFQDFPSKRYKDDQGHPCLNQGH 100  
 Qy 61 CKDOLQSYTCFCFLPAFEGRNCENHKDDOLICVNGGCEQYCSDHGTMKRSORCHEGSYL 120  
 Db 101 CKDQGIDYTCFCLEGFEFKCESTRE-ICSLDNGGDCDFCREERSEVR-CSCANGYVL 157  
 Qy 121 LADGVSCPTEVPGKIPILER----- 144  
 Db 158 GDDSKSCVSTERFPCKGFTQGRSRWAIHTSDALDASELHYDPDALSPRESSDILGL 217  
 Qy 145 NASPKQG-----RIVGGKVKPKGCOPWVLL-VNGAQLGGLINTIWVAHCF 195

Db	218	NRTPEPSAGEDSGQVVRVYVGGRDCAAEGCPWQALIUNNEENEGFCGGTILNEFVLTAAHCl	F;129-164/Domain: EGF homology <EG2> F;183-482/Product: coagulation factor X heavy chain #status predicted <HCH> F;183-231/Domain: activation peptide #status predicted <APT> F;232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT> F;232-460/Domain: trypsin homology <TRY>
Qy	196	DTKKNRLIAVLGHELDSEHDDCDEOSRRVAQVITPSPYVPGTTNHDITALLRHQPVLT	F;183-482/Domain: coagulation factor Xa heavy chain #status predicted <APT>
Db	278	HQAKRF--TVRGDNTTEQEGNEMAHENVMTVKHARFKETYDFIAVLRKTPRFR	F;232-482/Domain: coagulation factor Xa heavy chain #status predicted <ACT>
Qy	256	DHTVPCLPERFTSERLTFAVRPLSVLGWGLDGGATALEMLVNPRLMDQDCQQR	F;46-47, 54-56, 59-60, 65-66, 69-72, 79/Modified site: gamma-carboxyglutamic acid (Glu) F;57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-340, 238-243, 259-255, 388-400/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
Db	335	RIVAPACLPEKOWAETLMTOKTGIVSGFGTRHEKGRLSSTKLML3PYVDRSTC-----	F;187/Binding site: carbohydrate (Asn) (covalent) #status predicted F;208/Binding site: carbohydrate (Tyr) (covalent) #status predicted F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted F;231-232/Cleavage site: Arg-Tle (coagulation factor IXa, coagulation factor VIIa)
Qy	316	KVGDSPPNITEYMFAGYSDGSKSDCKGDGGATHAHRGTYLITGVWSWGCGATVGHFG	F;274, 320, 417/Active site: His, Asp, Ser #status predicted
Db	390	KLSSSTFTTPNMFCAISGTDQPDACGCDGGPHVTFPKDVFVTGIVSMWGCGCARKGKFG	449
Qy	376	VTRVSOVIVLWQLKMR	393
Db	450	VYTKVSNFLKWIDKINKA	467
RESULT 9			
EXRT			
C;Species	Rattus norvegicus (Norway rat)		
C;Date	31-Jan-1995	#sequence_revision	07-Feb-1997 #text_change 08-Dec-2000
C;Accession	SA9075; JC4670; PS0191; PS1190; I62745		
R;Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.			
R;Thromb. Res.	80, 63-73, 1995		
A;Title	Evidence for competition between vitamin K-dependent clotting factors for intracellular binding sites.		
A;Accession	A58498; MUID:96093366; PMID:8578539		
A;Molecule type	mRNA		
A;Residues	1-482 <STA1>		
A;Cross-references	EMBL:X79807; NID:9506600; PIDN:CHA56202.i; PID:9506601		
A;Note	Submitted to the EMBL Data Library, June 1994		
A;Note	Neither the complete nucleic acid sequence nor the complete translation are shown.		
R;Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.			
R;Gene	169, 269-273, 1996		
A;Title	Processing and expression of rat and human clotting factor-X-encoding cDNAs.		
A;Accession	JC4670		
A;Reference number	104298; MUID:96194815; PMID:8647460		
A;Molecule type	mRNA		
A;Residues	1-442 <STA2>		
A;Cross-references	EMBL:X79807; NID:9506600; PIDN:CHA56202.1; PID:9506601		
A;Residues	R;Enjoji, K.; Mizraki, K.; Kato, H.		
A;Title	Characterization of rat factors X and Xa: demonstration of factor Xa in rat platelets.		
A;Reference number	PS0190; MUID:92041742; PMID:1719494		
A;Accession	PS0191		
A;Molecule type	protein		
A;Residues	41-58, X, 60-65 <ENJ1>		
A;Accession	PS0190		
RESULT 10			
Qy	1	ANAFLXILRPESLXRLCKXXQGSEFXARXIKPDKXAMRPLKFLWNSYSDQDCASPCONGGS	60
Db	41	ANSFEPERIKKGNALERECVEETCSFEAREEVDNEKEPTFWKTYEDGQDCDSCPSQNGE	100
Qy	61	CKDQLOSYICVCLPAPAFGRNCETHKDQLICNENGCEQVCSQSDHTGKRSRCRGYSL	120
Db	101	CRDGJLSYTCCTCTEGFEGKNCLEFV--RKLCSDLNDQCDQCREEONSV VCSACKGYFL	157
Qy	121	LADGVSTCPTVYPCCKI-----	157
Db	158	GNDGRSCLSTRAPPCCGCKTNKRAKRSVALNTNSNSEPDPEIDLMPADILYPTESPBLNL	217
Qy	145	NASKPOG-----RIVGKVKPGKCPWPQVULLVNGAQ--LGGGLINTIWVNSAACFD	196
Db	218	NKTEPEANSDDVIRTVLGVQGCKBGPWPQWQNLFSBDTGCQGGTILNEVYLTAHCLH	277
Qy	197	KKNNRLIAVLGHELDSEHDDCDEOSRRVAQVITPSPYVPGTTNHDITALLRHQPVLT	256
Db	278	QAKRFK--TVRGDNTTEQEDGEGNHEVDMIKHKFQDITYDFIDAMILRKTPITRE	334
Qy	257	HVPLVCLPERFTSERLTFAVRPLSVLGWGLDGGATALEMLVNPRLMDQDCQQR	316
Db	335	NVAPACLPQDKWAEATLMTOKTGIVSGFGTRHEKGROSKVLMMEVYVYDRTC-----R	389
Qy	317	VGDSPPNITEYMFAGYSDGSKSDCKGDGGPHATHAHRGTYLITGVWSWGCGATVGHFG	376
Db	390	LSTSITONMFCAQYDAQOQDGGPHVIREKDYFVTGIVSMWGCGCARKGKFG	449
Qy	377	YTRVSOVIVLWQLKMRSEP	397
Db	450	YTKVTAFLKWIDRSMKARVGP	470
RESULT 11			
Qy	30419	JQ0419	
C;Species	Mus musculus (house mouse)		
C;Date	07-Sep-1990	#sequence_revision	07-Sep-1990 #text_change 16-Jul-1999
C;Accession	JQ0419; I49667		
R;Wu, S.M.; Stafford, D.W.; Ware, J.			
A;Status	preliminary		
A;Molecule type	DNA		
A;Residues	295-383, G' 395-455 <MUR>		
A;Cross-references	GB:D21215; NID:9415309; PIDN:BAA04756.1; PID:9455396		
A;CFunction			
A;Description	catalyzes the proteolytic activation of prothrombin to thrombin in the plasma		
A;Keywords	beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl		
A;Superfamily			
A;Pathway	blood coagulation		
A;Title	coagulation factor X: EGF homology; Gla domain homology; trypsin homology		
A;Accession	F;1-23/Domain: signal sequence #status predicted <SIG>		
A;Accession	F;24-40/Domain: propeptide #status predicted <PRO>		
A;Accession	F;25-84/Domain: Gla domain homology <GLA>		
A;Accession	F;41-79/Domain: coagulation factor X light chain #status predicted <LCX>		
A;Accession	F;90-121/Domain: EGF homology <EG1>		
A;Accession	I49667		
A;Status	preliminary; translated from GR/EMBL/DPB		
A;Accession	JQ0419		
A;Molecule type	mRNA		
A;Residues	1-459 <WU5>		
A;Cross-references	GB:M23109; NID:9193317; PIDN:AAA37629.1; PID:9387158		
A;Experimental source	liver		
A;Reference number	JQ0419; MUID:90215309; PMID:2323576		
R;Sarkar, G.; Koerner, D.D.; Sommer, S.S.			
C;Genomics	6, 133-143, 1990		
A;Title	direct sequencing of the activation peptide and the catalytic domain of the		
A;Reference number	I46580; MUID:90152675; PMID:2303254		
A;Accession	I49667		

A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-452 <AXE>  
A;Cross-references: GB:N38326; NID:9163949; PID:AAA30844\_1; PID:9163950  
C;Superfamily: coagulation factor X; EGFR homology; Gla domain homology; trypsin homolog  
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu  
F;1-21//Domain: signal sequence #status predicted <SIG>  
F;22-40//Domain: propeptide #status predicted <PRO>  
F;24-84//Domain: Gla domain homology <GIA>  
F;41-452//Product: coagulation factor IX #status predicted <MAT>  
F;90-121//Domain: EGFR homology <EGF1>  
F;127-163//Domain: BGF homology <BG2>  
F;218-45//Domain: trypsin homology <TRY>  
F;46,47,54,56,59,60,65,66,69,72,75,79//Modified site: gamma-carboxyglutamic acid (Glu)  
F;57-62,90-101,95-110,112-121,121-138,134-148,150-163,171-326,243-259,373-387,398-426  
F;258,306,402//Active site: His, Asp, Ser #status predicted

Db	274	RDPWLDIKKEVLLVHPNTYRNSNDIALLRSQATLSKTVIPCLPNSLQAELSQLA	60
Qy	276	VFRSLVSGWQGOLD-----ROTATELMVLVNPRLMTQDCQOSRKVGDSNITEYMF	329
Db	334	GOETVVTGWGICQSDKVKDGRNRRTFI-LTFIRIPLAARNDCQVMNNV---VSNNLC	387
Qy	330	AGYSDESKDSCKGDSGPCHATHYRGWYLIGIVSMQCATAVGHFGCVTRVSQVLENQK	389
Db	388	AGITGDPRDADCDDGSGCPMVVEFRGTWFLVGLYSWEGCGHHLNNYGVTKVGSYLNHS	447
Db	121	GSRDSCKGDSGGPHATRYGWTWLYLGIVSWGQCAVGH	159
RESULT 13			
S18994			
C;Species: Rattus norvegicus (Norway rat)			
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999			
C;Accession: S18994; S24312			
A;Description: The DNA cloning and mRNA expression of rat protein C.			
A;Reference number: S18994			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-461 <OKA>			
A;Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963			
A;Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963			
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology			
C;Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine protease			
C;Status: signal sequence #status predicted <SIG>			
F;27-85/Domain: Gla domain homology <GLA>			
F;33-42/Domain: Propeptide #status predicted <PRO>			
F;43-461/Domain: Protein C #status predicted <PRO>			
A;Title: The cDNA cloning and mRNA expression of rat protein C.			
A;Reference number: S18994; MUID:92319550; PMID:1621650			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-461 <OKA>			
A;Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963			
A;Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963			
A;Accession: S18994			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-461 <TRD>			
A;Cross-references: GB:D10445; NID:9220385; PIDN:BAA01235.1; PID:9220386			
A;Experimental source: liver			
A;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase th			
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology			
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxygl			
F;1-33/Domain: signal sequence #status predicted <GLA>			
F;27-85/Domain: Gla domain homology <GLA>			
F;34-41/Domain: propeptide #status predicted <PRO>			
F;42-196-199-461/Domain: protein C #status predicted <PRO>			
F;43-196/Domain: light chain #status predicted <RC1>			
F;91-130/Domain: EGF homology <EG>			
F;139-174/Domain: EGF homology <EG>			
F;199-461/Domain: heavy chain #status predicted <PCN>			
F;219-211/Domain: activation peptide #status predicted <ACT>			
F;212-461/Domain: protein K-dependent serine proteinase #status predicted <VKT>			
F;212-445/Domain: trypsin homology <TRY>			
F;47-48-55-57-60-61-66-67-70-76/Modified site: gamma-carboxyglutamic acid (Glu) #statu			
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted			
F;211-130-139-150-146-159-161-174-182-219-228-254-373-387-398-426/Disulfide bonds: #stat			
F;214-290-355/Binding site: carbohydrate (Asn) (covalent) #status predicted			
F;253-299-402/Active site: His, Asp, Ser #status predicted			
Query Match	35.4%	Score 775; DB 1; Length 461;	
Best Local Similarity	37.7%	Pred. No. 2.4e-50; Mismatches 156; Indels 48; Gaps 11;	
Matches	164;	Conservative 67; Mismatches 156; Indels 48; Gaps 11;	
1	ANAFLXXLRPGSLXRXCXQXXPSFXXKIFKDXAXTRFLWVSYSDQCAS-----	52	
42	ANSFLETRVAGSLEREMEEICDFEEQEIFQVNEDTIAFWKIKYFDGQCCSTPPLDHQCD	101	
53	SPCQNGGSKDKQDLSQYICFCFLPAFEGGNCETHKDQJLJVNEGCCQCSDHGTRSC	112	
102	SPCCGHGTCIDGLGFSCSDKRQWEGRCQEMGFO-DCRVKNGGCYHYCLEBTRGR-C	159	
113	RHEGYSLLADGVSCPTIVEYPCGKIPITLEKRKNASKQG-----RLVGG	156	
160	RKAPGYELADDHHMHCRTPVNFPCGK--LWKRDKKRKNFKRDPDEEELGPRTVNG	216	
157	KVQPKGCKPQWQVILLVNLVQL-CGGTINTIWIWSAHCDFDKTKRNWLAVLGEHDL	215	
217	TUJKQGSPWPQWILLLDKKKLACGGVVIHTSWLTAHCLESSK--KLIVRLGEYDLRR	273	
216	HQDDEOERRVAQVITPTPYCPTTNHIDALLRHOPPVLTDVHPVPLPERFSERTLAF	275	
RESULT 14			
JX0210			
Protein C (activated) (EC 3.4.21.69) precursor - mouse			
N:Alternate names: vitamin K-dependent serine proteinase			
C;Species: Mus musculus (house mouse)			
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000			
C;Accession: JX0210			
R;Rada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.			
J. Biochem. 111, 491-495, 1992			
A;Title: Isolation and characterization of a mouse protein C cDNA.			
A;Reference number: JX0210; MUID:92316897; PMID:1618739			
A;Accession: JX0210			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-461 <TRD>			
A;Cross-references: GB:D10445; NID:9220385; PIDN:BAA01235.1; PID:9220386			
A;Experimental source: liver			
A;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase th			
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology			
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxygl			
F;1-33/Domain: signal sequence #status predicted <GLA>			
F;27-85/Domain: Gla domain homology <GLA>			
F;34-41/Domain: propeptide #status predicted <PRO>			
F;42-196-199-461/Domain: protein C #status predicted <PRO>			
F;43-196/Domain: light chain #status predicted <RC1>			
F;91-130/Domain: EGF homology <EG>			
F;139-174/Domain: EGF homology <EG>			
F;199-461/Domain: heavy chain #status predicted <PCN>			
F;219-211/Domain: activation peptide #status predicted <ACT>			
F;212-461/Domain: protein K-dependent serine proteinase #status predicted <VKT>			
F;212-445/Domain: trypsin homology <TRY>			
F;47-48-55-57-60-61-66-67-70-76/Modified site: gamma-carboxyglutamic acid (Glu) #statu			
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted			
F;211-130-139-150-146-159-161-174-182-219-228-254-373-387-398-426/Disulfide bonds: #stat			
F;214-290-355/Binding site: carbohydrate (Asn) (covalent) #status predicted			
F;253-299-402/Active site: His, Asp, Ser #status predicted			
Query Match	35.2%	Score 769; DB 1; Length 461;	
Best Local Similarity	36.9%	Pred. No. 6.8e-50; Mismatches 159; Indels 42; Gaps 12;	
Matches	164;	Conservative 80; Mismatches 159; Indels 42; Gaps 12;	
1	ANAFLXXLRPGSLXRXCXQXXPSFXXKIFKDXAXTRFLWVSYSDQCAS-----	52	
42	ANSFLETRVAGSLEREMEEICDFEEQEIFQVNEDTIAFWKIKYFDGQCCSTPPLDHQCD	101	
53	SPCQNGGSKDKQDLSQYICFCFLPAFEGGNCETHKDQJLJVNEGCCQCSDHGTRSC	112	
102	SPCCGHGTCIDGLGFSCSDKRQWEGRCQEMGFO-DCRVKNGGCYHYCLEBTRGR-C	159	
113	RHEGYSLLADGVSCPTIVEYPCGKIPITLEKRKNASKQG-----RLVGG	156	
160	RKAPGYELADDHHMHCRTPVNFPCGK--LWKRDKKRKNFKRDPDEEELGPRTVNG	216	
157	KVQPKGCKPQWQVILLVNLVQL-CGGTINTIWIWSAHCDFDKTKRNWLAVLGEHDL	215	
217	TUJKQGSPWPQWILLLDKKKLACGGVVIHTSWLTAHCLESSK--KLIVRLGEYDLRR	273	
216	HQDDEOERRVAQVITPTPYCPTTNHIDALLRHOPPVLTDVHPVPLPERFSERTLAF	275	
RESULT 15			
QY	276	VFRSLVSGWQGOLD-----ROTATELMVLVNPRLMTQDCQOSRKVGDSNITEYMF	329
Db	334	GOETVVTGWGICQSDKVKDGRNRRTFI-LTFIRIPLAARNDCQVMNNV---VSNNLC	387
Qy	330	AGYSDESKDSCKGDSGPCHATHYRGWYLIGIVSMQCATAVGHFGCVTRVSQVLENQK	389
Db	388	AGITGDPRDADCDDGSGCPMVVEFRGTWFLVGLYSWEGCGHHLNNYGVTKVGSYLNHS	447
Qy	390	LMRSEPRPGVLLRAP 404	
Db	448	YIGER---DVSKSP 459	

Db 277 ELDLIDKEILVHRYTRSSSDNIDALLRQAMLSKTVIPCLPNNGLAQMLLTQGQE 336  
 Qy SIVSGNGQLDQ---RGATLLEMLNVPRIMTQCLOQSRRKVGDSPNITYEMFCAGY 332  
 Db 337 TVTGVGYQOSDRIKDGRRNRPTI-LAFTRIPAVRNECVEVKY---VSENMLCAGI 390  
 Qy 333 SDGSKSCKGGSGGPHATHYRWTWILGIVSNGQCATVGHCYVTRSQYEWLQLMR 392  
 Db 391 IGNTRADCGDGGPMPVFRGTFWLGLVSNEGCQHTNNYGYITKVGSIWKIHSIG 450  
 Qy 393 SEPPPGVLRA 403  
 ; ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 451 EK--GVSLSK 458

## RESULT 15

KXBO protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Accession: A2-Nov-1980 #sequence\_revision 17-Mar-1987 #text\_change 16-Jul-1999  
 R;Long, G.L.; Baladeje, R.M.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984  
 A;Title: Cloning and sequence of liver cDNA coding for bovine protein C.  
 A;Reference number: A26250; MUID:85014826; PMID:6091100  
 A;Molecule type: mRNA  
 A;Residues: 1-456 <LON>  
 R;Fernlund, P.; Stenflo, J.  
 J. Biol. Chem. 257, 12170-12179, 1982  
 A;Title: Amino acid sequence of the light chain of bovine protein C.  
 A;Reference number: A18385; MUID:83007325; PMID:6896876  
 A;Molecule type: protein  
 A;Residues: 40-194 <FER>  
 A;Note: 82-LYS was also found  
 R;Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983  
 A;Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.  
 A;Reference number: A19316; MUID:83169769; PMID:6572939  
 A;Contents: annotation; revision to residue 110  
 R;Stenflo, J.; Fernlund, P.; Drakenberg, T.  
 J. Biol. Chem. 257, 12180-12190, 1982  
 A;Title: Amino acid sequence of the heavy chain of bovine protein C.  
 A;Accession: A18386  
 A;Molecule type: protein  
 A;Residues: 197-454, 'PV' <SPE>  
 R;Emson, N.L.; Debault, L.E.; Emson, C.T.  
 J. Biol. Chem. 258, 5548-5553, 1983  
 A;Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F  
 A;Reference number: A37541; MUID:83211513; PMID:630092  
 A;Contents: annotation; activation; calcium binding  
 R;Johnson, A.E.; Emson, N.L.; Lane, T.M.; Emson, C.T.  
 J. Biol. Chem. 256, 5554-5560, 1983  
 A;Title: Structural changes required for activation of protein C are induced by Ca<sup>2+</sup> bin  
 A;Reference number: A37542; MUID:83213514; PMID:6406503  
 A;Contents: annotation; activation; calcium binding  
 C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re  
 b. C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is cleaved by a tetrapeptidase from the amino end of the heavy chain; this reaction requires calcium binding to the gamma-carboxyglutamic acid (Gla) residues and, with structural cognition of the thrombin-thrombomodulin complex.  
 C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin C;Supfamily: coagulation factor X; EGF homology; Gla domain homology; trytein homology; blood coagulation; calcium binding  
 C;Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding  
 F;1-29/Domain: signal sequence (fragment) #status predicted <SIG>  
 F;24-83/Domain: Gla domain homology <GLA>  
 F;30-39/Domain: propeptide #status predicted <PRO>  
 F;40-194/Domain: protein C light chain #status experimental <LC>

F;98-128/Domain: EGF homology <EG1>  
 F;137-172/Domain: EGF homology <EG2>  
 F;197-456/Domain: protein C heavy chain #status experimental <HC>  
 F;197-210/Domain: activation peptide #status experimental <AP>  
 F;211-440/Domain: trypsin homology <TR>  
 F;45,46,53,55,58,59,67,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #  
 F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental <AS>  
 F;119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #  
 F;136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Best Local Similarity 34.2%; Score 749; DB 1; Length 456; Matches 164; Conservative 63; Mismatches 157; Indels 40; Gaps 12; Query 1 ANAFLXXLRPGSLXKRXKXXOCFSXXARXKIFKDAXRTKLFWISYSDGDOC-----AS 52  
 Db 40 ANSFLESLRPGUNVERCSECEAREINTONEDPMARFSYSDGDOCDDPSSPC 99  
 Qy 53 SPCQNGGSCCKDOLQSYTCFCFLPAFGRNCRTHKDDOLICNGCSEQYSDHGTKRSC 112  
 Db 100 LPCCGRCKCIDOLGGFRCDCAEGWEGRPC\_LHEVRFNSNCSAENGCAHYCMEEG\_RRHC 157  
 Qy 113 RCHEGYVLLADCVSCTPVEPGKLI-PILKRNAs-----KPO--GRIVGGKVC 159  
 Db 158 SCAPGIRLEDDHQLCYSKVTFFPCGRLGRKMERKKRKLDPDNQVQDKDQDLPRTDQGQA 217  
 Qy 160 PKGECPIKQVLLVNGQLCGFTLIMIWIWVAACFDFKIKNWRNLIAVGEHDSEHDG 218  
 Db 218 GWGESPMQVAVIDLSSKRLKVVCAVLLVWVNTVANLDSK--KLIVRGGEYDRRMWS 274  
 Qy 219 DEQSRVVAQWIPSTIVPGTNHDALLRKHOPVWTDHVPLCLPRTSERTLAFV-R 277  
 Db 275 WEVLDLKEVTHPNYTKSTSNDNIALRLLAKPALSQTIVPCLPDSGLSERKLTVQGQ 334  
 Qy 278 FSLVSGNGQLDRGAT---ALELMYLNVPRLMTDCLOCSRSKVGDSPNTEYNECAGS 333  
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:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| 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Search completed: July 1, 2003, 17:54:33  
 Job time : 43 secs